OM nucleic - nucleic search, using sw model

January 13, 2003, 22:19:33; Search time 5440 Seconds Run on:

(without alignments)

11154.292 Million cell updates/sec

US-09-846-589A-9 Title:

2085 Perfect score:

1 ggaaaccgtgtttcgacggg.....tatacttgacagttgactcc 2085 Sequence:

Scoring table: OLIGO NUC

Gapop 60.0 , Gapext 60.0

2054640 seqs, 14551402878 residues Searched:

Word size :

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

GenEmbl:* Database :

1: gb ba:*

2: gb_htg:*

3: gb_in:*

4: gb om:*

5: gb_ov:*

6: gb pat:*

7: gb_ph:*

8: gb_pl:* 9: gb pr:*

10: gb_ro:*

11: gb sts:*

12: gb_sy:*

13: gb un:*

14: gb vi:*

15: em ba:*

16: em fun:*

17: em hum:*

18: em in:*

19: em mu:*

20: em om:*

em_or:* 21:

22: em ov:*

23: em pat:*

24: em ph:*

25: em pl:*

26: em_ro:*

27: em_sts:* Sog Search Surumany for Leg 9 Oligo

```
28: em_un:*
29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

			96			SUMMARIES		6255090
Resi	ılt		Query				USPIO	
	10.	Score		Length	DB	ID	<i>!</i> . _	Description
	1	2085	100.0	2085	6	AR160636		AR160636 Sequence
	2	32	1.5	1957	6	AR160637		AR160637 Sequence
	3	32	1.5	142373	2	AC122149		AC122149 Oryza sat
	4	32	1.5	261604	2	AC119819		AC119819 Mus muscu
С	5	32	1.5	261604	2	AC119819		AC119819 Mus muscu
	6	25	1.2	242	9	AF023663		AF023663 Macaca ra
	7	25	1.2	5737	3	DMU78088		U78088 Drosophila
С	8	25	1.2	8718	6	AX346174		AX346174 Sequence
	9	25	1.2	22578	2	AC015113		AC015113 Drosophil
С	10	25	1.2	80692	2	AC100569		AC100569 Mus muscu
С	11	25	1.2	86209	8	AP004523		AP004523 Lotus jap
	12	25	1.2	87767	2	AC014497		AC014497 Drosophil
	13	25	1.2	90608	2	AC128541		AC128541 Rattus no
	14	25	1.2	146893	2	CNS08C9A		AL732535 Oryza sat
•	15	25	1.2	150347	2	AC027038		AC027038 Oryza sat
С	16	25	1.2	150587	3	AC007549		AC007549 Drosophil
С	17	25	1.2	179421	2	AC110690		AC110690 Rattus no
С	18	25	1.2	181771	3	AC008340		AC008340 Drosophil
С	19	25	1.2	187437	3	AC023751		AC023751 Drosophil
С	20	25	1.2	188781	10	AL713870		AL713870 Mouse DNA
С	21	25	1.2	215986	9	AP002379		AP002379 Homo sapi
С	22	25	1.2	301769	3	AE003482		AE003482 Drosophil
С	23	24	1.2	341	6	AX397195		AX397195 Sequence
	24	24	1.2	5671	3	AY119457		AY119457 Drosophil
	25	24	1.2	9700	9	AB032251		AB032251 Homo sapi
С	26	24	1.2	14947		AC014403		AC014403 Drosophil
	27	24	1.2	33038	3	U97016		U97016 Caenorhabdi
С	28	24	1.2	59843	8	AP000816		AP000816 Oryza sat
	29	24	1.2	62091	2	DMBR28018		AL121814 Drosophil
	30	24	1.2	71154		AC130323		AC130323 Homo sapi
	31	24	1.2	80692		AC100569		AC100569 Mus muscu
С	32	24		111191		AC127525		AC127525 Homo sapi
	33	24	1.2	119526	2	AC007468		AC007468 Drosophil

OM nucleic - nucleic search, using sw model

January 13, 2003, 20:47:02; Search time 436 Seconds Run on:

(without alignments)

10769.304 Million cell updates/sec

US-09-846-589A-9 Title:

Perfect score:

1 ggaaaccgtgtttcgacggg.....tatacttgacagttgactcc 2085 Sequence:

Scoring table: OLIGO NUC

Gapop 60.0 , Gapext 60.0

2185239 seqs, 1125999159 residues Searched:

Word size :

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

N Geneseg 101002:* Database :

1: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:*

2: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*

3: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1982.DAT:*

4: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1983.DAT:*

/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1984.DAT:*

/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1985.DAT:*

/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1986.DAT: * 7:

8: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1987.DAT:*

9: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1988.DAT:*

10: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1989.DAT:*

/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1990.DAT:* 11:

/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1991.DAT:* 12:

/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1992.DAT:* 13:

/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1993.DAT:* 14:

/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1994.DAT:* 15:

/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1995.DAT:* 16:

/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1996.DAT:* 17:

18: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1997.DAT:*

/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1998.DAT:* 19:

/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1999.DAT:* 20:

/SIDS2/gcgdata/geneseq/geneseqn-embl/NA2000.DAT:* 21:

/SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:* 22:

/SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:* 23:

/SIDS2/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

JEPN 6255090

5	SUMMARIES	

_			8				from	
Res			Query		D.D.	T.D.	, R -	Description
1	No.	Score	Match	Length	DB	ID	/ \	Description
	1	2005	100 0	2085	22	AAD07973		Corn cysteinyl-tRN
	1	2085	100.0	2083	24	ABL72570		Corn tassel-derive
	2	112	5.4					
	3	32	1.5	1957	22	AAD07974		Rice cysteinyl-tRN
С	4	25	1.2	902	24	ABQ46430		Oligonucleotide fo
	5	25	1.2	902	24	ABQ46431		Oligonucleotide fo
С	6	25	1.2	8718	24	ABL33272		Human immune syste
С	7	25	1.2	28360	23	ABL06142		Drosophila melanog
С	8	24	1.2	341	24	ABK45859		cDNA encoding colo
С	9	24	1.2	903	24	ABQ14804		Oligonucleotide fo
	10	24	1.2	903	24	ABQ14805		Oligonucleotide fo
	11	24	1.2	9700	21	AAZ39033		Human transcriptio
	12	24	1.2	9865	21	AAZ39032		Human transcriptio
	13	24	1.2	10314	23	ABL29797		Drosophila melanog
	14	24	1.2	13560	23	ABL28568		Drosophila melanog
	15	24	1.2	17729	23	ABL29796		Drosophila melanog
С	16	23	1.1	578	24	ABQ36480		Oligonucleotide fo
	17	23	1.1	578	24	ABQ36481		Oligonucleotide fo
С	18	23	1.1	12425	22	AAH26495		Human low density
С	19	23	1.1	14568	24	ABL32230		Human immune syste
С	20	23	1.1	14686	23	ABL15140		Drosophila melanog
	21	23	1.1	23710	23	ABL08132		Drosophila melanog
С	22	23	1.1	29329	22	ABA18026		Human nervous syst
C	23	23	1.1	29329	22	ABA20511		Human nervous syst
C	24	23	1.1	29329	22	AAK70791		Human immune/haema
c	25	23	1.1	29329	22	AAK78512		Human immune/haema
	26	22		494	21	AAC51742		Zea mays DNA fragm
С	27	22	1.1	586	24	ABQ50526		Oligonucleotide fo
Ŭ	28	22	1.1	586	24	ABQ50527		Oligonucleotide fo
С	29	22	1.1	796	24	ABQ28404		Oligonucleotide fo
C	30	22	1.1	796	24	ABQ28405		Oligonucleotide fo
С	31	22	1.1	958	24	ABQ43126		Oligonucleotide fo
C	32	22	1.1	958	24	ABQ43127		Oligonucleotide fo
0	33	22	1.1	1147	24	ABQ42108		Oligonucleotide fo
С	34	22	1.1	1147	24	ABQ42100 ABQ42109		Oligonucleotide fo
_	35	22		1341	24	ABQ15050		Oligonucleotide fo
С	36		1.1		24			-
	36 37	22 22	1.1	1341	21	ABQ15051 AAC44491		Oligonucleotide fo
_		22		1600				Zea mays DNA fragm
С	38		1.1	1618	24	ABQ39530		Oligonucleotide fo
	39	22	1.1	1618	24	ABQ39531		Oligonucleotide fo
_	40	22	1.1	2366	22	AAK51465		Human polynucleoti
С	41	22	1.1	2406	22	AAK52449		Human polynucleoti
С	42	22	1.1	2500	24	ABN95898		Gene #2396 used to
С	43	22	1.1	2500	24	ABK72303		Lymphona associate
С	44	22	1.1	5391	24	ABK39939		Human chemically p
С	45	22	1.1	5391	24	ABL32243		Human immune syste

OM nucleic - nucleic search, using sw model

Run on: January 13, 2003, 20:59:21; Search time 81 Seconds

(without alignments)

7894.087 Million cell updates/sec

Title: US-09-846-589A-9

Perfect score: 2085

Sequence: 1 ggaaaccgtgtttcgacggg.....tatacttgacagttgactcc 2085

Scoring table: OLIGO NUC

Gapop 60.0 , Gapext 60.0

Searched: 441362 seqs, 153338381 residues

Word size: 0

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents_NA:*

1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*

3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*

5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Resi	ult No.	Score	% Query Match	Length	DB	ID	Description
	1	2085	100.0	2085	4	US-09-352-990-9	Sequence 9, Appli
	2	32	1.5	1957	4	US-09-352 - 990-11	Sequence 11, Appl
	3	21	1.0	333	1	US-08-844-010-3	Sequence 3, Appli
	4	21	1.0	333	3	US-09-012-873-3	Sequence 3, Appli
	5	21	1.0	451	4	US-09-357-251-3	Sequence 3, Appli
С	6	21	1.0	640	2	US-08-835-099A-16	Sequence 16, Appl
С	7	21	1.0	640	3	US-09-157-349-16	Sequence 16, Appl
С	8	21	1.0	804	2	US-08-835-099A-10	Sequence 10, Appl
С	9	21	1.0	804	3	US-09-157-349-10	Sequence 10, Appl
	10	21	1.0	1070	4	US-09-470-443-7	Sequence 7, Appli
	11	21	1.0	1344	1	US-08-844-010-1	Sequence 1, Appli
	12	21	1.0	1344	3	US-09-012-873-1	Sequence 1, Appli

OM nucleic - nucleic search, using sw model

Run on: January 13, 2003, 22:30:12; Search time 97 Seconds

(without alignments)

9459.953 Million cell updates/sec

Title: US-09-846-589A-9

Perfect score: 2085

Sequence: 1 ggaaaccgtgtttcgacggg.....tatacttgacagttgactcc 2085

Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 389086 seqs, 220051671 residues

Word size : 0

Total number of hits satisfying chosen parameters: 778172

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published Applications_NA:*

1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*

2: /cgn2 6/ptodata/2/pubpna/PCT NEW PUB.seq:*

3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*

4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*

5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*

6: /cgn2 6/ptodata/2/pubpna/PCTUS PUBCOMB.seq:*

7: /cgn2 6/ptodata/2/pubpna/US08_NEW_PUB.seq:*

8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*

9: /cgn2 6/ptodata/2/pubpna/US09 NEW PUB.seq:*

10: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*

11: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*

12: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*

13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Re	esult No.		Score	% Query Match	Length	DB	ID	Description	1 	- -
•	<u>-</u>		249	11.9	249	10		Sequence	•	-
	2	2	112	5.4	294	10	US-09-294-093B-1944	Sequence	1944,	Аp
(c 3	3	24	1.2	341		00 00 000	Sequence	1410,	Аp
(٠	1	2.4	1.2	341	12	US-10-033-528-1410	Sequence	1410,	Аp

OM nucleic - nucleic search, using sw model

Run on: January 13, 2003, 22:25:37; Search time 2958 Seconds

(without alignments)

11415.683 Million cell updates/sec

Title: US-09-846-589A-9

Perfect score: 2085

Sequence: 1 ggaaaccgtgtttcgacggg.....tatacttgacagttgactcc 2085

Scoring table: OLIGO NUC

Gapop 60.0 , Gapext 60.0

Searched: 16154066 seqs, 8097743376 residues

Word size: 0

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : EST:*

1: em_estba:*
2: em_esthum:*
3: em_estin:*

4: em_estmu:*
5: em_estov:*
6: em_estpl:*

7: em_estro:* 8: em_htc:*

9: gb_est1:* 10: gb_est2:*

11: gb_est2:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*
15: em estfun:*

16: em_estom:*

17: gb gss:*

.18: em gss hum:*

19: em gss_inv:*

20: em_gss_pln:*

21: em_gss_vrt:*

22: em_gss_fun:*

23: em_gss_mam:*

24: em_gss_mus:*

25: em gss other:*

26: em gss pro:*

27: em gss rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

							SUMMARIE	12
				8				
	Res	ult		Query				
	1	No.	Score	Match 1	Length 1	DB	ID	Description
		 1	2085	100.0	2120	 11	AY104190	AY104190 Zea mays
	0	2	566	27.1	577	10	AW000193	AW000193 614058H08
	С	3	521	25.0	624	10	AW065367	AW065367 614048G06
		4	505	24.2	581	10	AW065368	AW065368 614048G07
		5	452	21.7	636	10	AW065483	AW065483 614058H08
	_	6	419	20.1	470		AI947463	AI947463 614048G07
	С	7	387	18.6	586	10	AW563004	AW563004 660070H04
		8	368	17.6	451	13	BM498280	BM498280 952021B05
			365	17.5	548	13	BM498016	BM498016 952021B05
		9 10	337	16.2	522	13	BM428660	BM428660 952021B05
	_		337	16.2	548	14	BQ667878	BQ667878 946101G05
	С	11 12	328	15.7	478	14	BQ667879	BQ667879 946101G05
	_		290	13.7	594	10	AW600543	AW600543 660070H04
	С	13			604	9	AI746204	AI746204 605082F05
	С	14	272	13.0		10	AW497943	AW497943 660042A12
		15	236	11.3	588		AW497943 AW498128	AW498128 660042A12
	С	16	233	11.2	504	10	AW498128 AI939893	AI939893 618026C01
	С	17	174	8.3	327	9	BQ778947	BQ778947 946115G02
A.		18	160	7.7	393	14	BH412384	BH412384 1007026G1
entagi	, с	19	144	6.9	207	17		BQ282680 WHE3080 D
G)		20	113		412	14	BQ282680 BE593605	BE593605 WS1 98 F1
=	*9	21	113	5.4	547	10	AI649625	AI649625 486068G03
7	$\mathcal{E}_{\overline{a}}$	22	104	5.0	508	9		BH635759 1008006G1
0	4 c	23	99	4.7	484	17	BH635759	BQ294221 1091026H1
	**	24	96	4.6	584	14	BQ294221	BG411263 EM1 27 F0
2	SL	25	92	4.4	535	12	BG411263	AI622640 486105A09
2.	. 0 c	26	65	3.1	615	9	AI622640	BQ282168 WHE3055 F
\sim	4	27	54	2.6	359	14	BQ282168	AW286571 LG1_334_E
	1	28	54	2.6	478	10	AW286571	AW286571 LG1_334_L AW286552 LG1 334 C
34	61	29	54	2.6	533	10	AW286552	AW286332 LG1_334_C AW679266 WS1 23 HO
12.	S)	30	54	2.6	566	10	AW679266	BE593197 WS1 98 F1
hits long	•	31	54	2.6	647	10	BE593197	BE393197 W31_98_F1 BG411643 EM1 59 H0
_ =	2	32	52	2.5	253	12	BG411643	AI600795 486068G03
0	C	33	43	2.1	338	9	AI600795	AW679193 WS1 23 HO
5		34	41	2.0	244	10	AW679193	BG410925 EM1 27 F0
		35	37	1.8	590	12	BG410925	AV833385 AV833385
		36	35	1.7	609	10	AV833385	BM135900 WHE2619 H
		37	35	1.7	614	13	BM135900	BJ463548 BJ463548
		38	35	1.7	643	13		
	С	39	32	1.5	475	17	AZ858962	AZ858962 2M0164C22 BQ839424 WHE4165 H
		40	32	1.5	500	14	BQ839424	BQ839424 WHE4165_H BE497913 WHE0958 G
		41	32	1.5	502	10		BE497913 WHE0958_G BJ245810 BJ245810
		42	32	1.5	589	13		BE499567 WHE0962 H
		43	32	1.5	598	10	BE499567	BQ838563 WHE2912 A
		44	32	1.5	653	14		BQ838563 WHE2912_A AZ859302 2M0164C22
		45	30	1.4	600	17	AZ859302	AZ8593UZ ZMU164CZZ

OM nucleic - nucleic search, using sw model

January 13, 2003, 18:25:41; Search time 5450 Seconds Run on:

(without alignments)

11133.826 Million cell updates/sec

US-09-846-589A-9 Title:

Perfect score: 2085

1 ggaaaccgtgtttcgacggg.....tatacttgacagttgactcc 2085 Sequence:

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

2054640 seqs, 14551402878 residues Searched:

4109280 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

GenEmbl:* Database :

1: gb ba:*

2: gb htg:*

3: gb in:*

4: gb om:*

5: gb ov:*

6: gb pat:*

7: gb ph:*

8: gb pl:*

9: gb pr:*

10: gb ro:*

11: gb sts:*

12: gb sy:*

13: gb un:*

14: gb_vi:*

15: em ba:*

16: em fun:*

17: em hum:*

18: em in:*

19: em mu:*

20: em om:*

21: em_or:*

22: em_ov:*

23: em pat:*

24: em ph:*

25: em pl:*

27: em sts:*

26: em ro:*

Seg Search Summary for Seg ID No:9 (Identity)

```
28: em_un:*
29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Re	sult		% Query				
	No.	Score		Length	DB	ID	Description
-	 1	2085	100.0	2085	- -	AR160636	AR160636 Sequence
	2	1141.4	54.7	1957	6	AR160637	AR160637 Sequence
	3	456.2	21.9	2183	6	AR160638	AR160638 Sequence
	4	442.6	21.2	1867	8	AF370143	AF370143 Arabidops
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	11	275.6		304290	1	CNSPAX05	AJ248287 Pyrococcu
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	14	268.8	12.9	1922	1	BSCTS	X73989 B.subtilis
	15	268.8	12.9	6357	1	BACGLUSYN	L14580 Bacillus su
	16	268.8	12.9	180136	1	BAC180K	D26185 B. subtilis
	17	268.8	12.9	213080	1	BSUB0001	Z99104 Bacillus su
	18	267.2	12.8	92407	6	AX067461	AX067461 Sequence
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С	20	262.2	12.6	205050	1	AJ414155	AJ414155 Yersinia
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	22	255.2	12.2	15086	1	CST130879	AJ130879 Clostridi
С	23	254.6	12.2	10461	1	U32693	U32693 Haemophilus
	24	253.2	12.1	1416	6	AX413912	AX413912 Sequence
	25	253.2	12.1	160050	1	AL591974	AL591974 Listeria
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	28	251.6	12.1	1401	6	A93879	A93879 Sequence 1
	29	251.6	12.1	1401	6	AR016529	AR016529 Sequence
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	31	251.6		301050	1	AP003130	AP003130 Staphyloc
	32	251.6		325350	1	AP004823	AP004823 Staphyloc
	33	251.6	12.1	343590	1	AP003359	AP003359 Staphyloc

С	34	251.4	12.1	3242	1	AF269691	AF269691 Staphyloc
С	35	251.4	12.1	3242	6	AX145011	AX145011 Sequence
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С	37	250.2	12.0	11541	1	AE007813	AE007813 Clostridi
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ALIGNMENTS

RESULT 1 AR160636 LOCUS AR160636 2085 bp DNA linear PAT 17-OCT-2001 Sequence 9 from patent US 6255090. DEFINITION AR160636 ACCESSION VERSION AR160636.1 GI:16224963 KEYWORDS SOURCE Unknown. ORGANISM Unknown. Unclassified. REFERENCE (bases 1 to 2085) **AUTHORS** Famodu, L.O., Orozco, E.M. Jr. and Rafalski, J. Antoni. Plant aminoacyl-tRNA synthetase TITLE **JOURNAL** Patent: US 6255090-A 9 03-JUL-2001; FEATURES Location/Qualifiers 1. .2085 source /organism="unknown" BASE COUNT 603 a 466 c 501 g 515 t ORIGIN 100.0%; Score 2085; DB 6; Length 2085; Query Match Best Local Similarity 100.0%; Pred. No. 0; Matches 2085; Conservative 0; Mismatches 0; Indels Gaps 0; Qу 1 GGAAACCGTGTTTCGACGGGCCGCAGTGGGCAGTGGCTTGGCCCATCGAACCCACTTGCC 60 Db 1 GGAAACCGTGTTTCGACGGGCCGCAGTGGGCAGTGGCCTTGGCCCATCGAACCCACTTGCC 60 61 ACTCACTTCCACCTGAACTTTGCCCTGCCTTCTCTCGACGACTCCCCTGTCCCCGCCGCC 120 Qу Db 61 ACTCACTTCCACCTGAACTTTGCCCTGCCTTCTCTCGACGACTCCCCTGTCCCCGCCGCC 120 Qу 121 GCCGCCGCCAAATCCCCTTCCGCGTCTGTCTGGCCTCTGGGGCTTCTAGGTTAGCGCG 180 121 GCCGCCGCGCAAATCCCCTTCCGCGTCTGTCTGGCCTCTGGGGCTTCTAGGTTAGCGCG 180 Db Qy 181 TGCGACCACCATGGCCGAGGAGGTCCAGGCTCCACTTTCCGCCACCATGGCGAAGGAGGC 240

181 TGCGACCACCATGGCCGAGGAGGTCCAGGCTCCACTTTCCGCCACCATGGCGAAGGAGGC 240

Db

OM nucleic - nucleic search, using sw model

Run on: January 13, 2003, 17:24:05; Search time 437 Seconds

(without alignments)

10744.660 Million cell updates/sec

Title: US-09-846-589A-9

Perfect score: 2085

Sequence: 1 ggaaaccgtgtttcgacggg.....tatacttgacagttgactcc 2085

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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OM nucleic - nucleic search, using sw model

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; Patent No. 6255090
; GENERAL INFORMATION:
; APPLICANT: Famodu, Layo O.
; APPLICANT: Orozco, Buddy
; APPLICANT: Rafalski, Antoni
; TITLE OF INVENTION: Plant Aminoacyl-tRNA Synthetase
; FILE REFERENCE: BB-1191
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Perfect score: 2085

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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ALIGNMENTS

cited to PTO-892

RESULT 1 US-09-294-093B-1944

; Sequence 1944, Application US/09294093B

; Patent No. US20010051335A1

; GENERAL INFORMATION:

; APPLICANT: Lalgudi, Raghunath, V.

; APPLICANT: Ito, Laura, Y.

; APPLICANT: Sherman, Bradley, K.

; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN TASSEL

; FILE REFERENCE: PL-0009 US

OM nucleic - nucleic search, using sw model

Run on: January 13, 2003, 19:16:51; Search time 2957 Seconds

(without alignments)

11419.543 Million cell updates/sec

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Post-processing: Minimum Match 0%

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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